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SEQUENCE LISTING

<110> Agriculture Victoria Services Pty Ltd AND Pig Research and Development Corporation

<120> Novel lawsonia spp. gene and uses therefor II

<130> p:\oper\mro\lawson-2.pct

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<150> US 60/133,982

<151> 1999-05-12

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 186

<212> PRT

<213> Lawsonia intracellularis

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5

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25

30

Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys

35

40

45

Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala

50

55

60

Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala

65

70

75

80

Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu

85

90

95

Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu

100

105

110

Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu

115

120

125

Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp

130

135

140

Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr

- 2 -

Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
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Lys Leu Pro Glu Met Ala Asn Arg Lys Lys
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Ala Asn Ser Ala Phe Ser Ala Asp Phe Pro Ile Gly Val Phe Asn Ser
20 25 30

caa tcc att gcc atg gag agt gaa gca gct aag gcc gct caa aaa aaa 144
Gln Ser Ile Ala Met Glu Ser Glu Ala Ala Lys Ala Ala Gln Lys Lys
35 40 45

tta caa tca gaa ttt ggt aat gaa aaa aca caa ctt gaa aaa caa gca 192
Leu Gln Ser Glu Phe Gly Asn Glu Lys Thr Gln Leu Glu Lys Gln Ala
50 55 60

aaa gat ttg caa aca aaa gct gat gat tta caa gct aag tca gca gct 240
Lys Asp Leu Gln Thr Lys Ala Asp Asp Leu Gln Ala Lys Ser Ala Ala
65 70 75 80

atg tct aac caa gca cgt gaa gat aaa caa aga gaa ttt ctt gaa ctt 288
Met Ser Asn Gln Ala Arg Glu Asp Lys Gln Arg Glu Phe Leu Glu Leu
85 90 95

cgt cgt aat ttc gaa gaa aaa tct cgt gac ttt gca ata cgt gtc gaa 336
Arg Arg Asn Phe Glu Glu Lys Ser Arg Asp Phe Ala Ile Arg Val Glu
100 105 110

- 3 -

caa gct gaa aac aca tta cgt caa tat cta gct gaa caa acc tat ctt 384
Gln Ala Glu Asn Thr Leu Arg Gln Tyr Leu Ala Glu Gln Ile Tyr Leu
115 120 125

gct gct gaa act ata gca aaa aag aaa ggg tta aaa ctt gtt ctt gat 432
Ala Ala Glu Thr Ile Ala Lys Lys Lys Gly Leu Lys Leu Val Leu Asp
130 135 140

agt gct agt gga agt gta atg tac ctt gaa aaa sat cta gat att aca 480
Ser Ala Ser Gly Ser Val Met Tyr Leu Glu Lys Asn Leu Asp Ile Thr
145 150 155 160

aaa gaa att ctt gaa gcc ata aat gct gca tgg aaa aaa ggt gga agt 528
Lys Glu Ile Leu Glu Ala Ile Asn Ala Ala Trp Lys Lys Gly Gly Ser
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